

SEQUENCE LISTING

<110> Sims, John
Born, Theresa

<120> ACPL DNA and Polypeptides

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<140> 09/616,530

<141> 2000-07-14

<150> PCT/US99/01420

<151> 1999-01-22

<150> 60/078,835

<151> 1998-03-20

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<170> PatentIn version 3.4

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Asn	Ile	Ile	Leu	Glu	Lys	Val	Thr	Gln	Arg	Asp	Leu	Arg	Arg	Lys	Phe	
320					325					330					335	
gtt	tgc	ttt	gtc	cag	aac	tcc	att	gga	aac	aca	acc	cag	tcc	gtc	caa	1536
Val	Cys	Phe	Val	Gln	Asn	Ser	Ile	Gly	Asn	Thr	Thr	Gln	Ser	Val	Gln	
				340					345					350		
ctg	aaa	gaa	aag	aga	gga	gtg	gtg	ctc	ctg	tac	atc	ctg	ctt	ggc	acc	1584
Leu	Lys	Glu	Lys	Arg	Gly	Val	Val	Leu	Leu	Tyr	Ile	Leu	Leu	Gly	Thr	
			355					360					365			
atc	ggg	acc	ctg	gtg	gcc	gtg	ctg	gcg	gcg	agt	gcc	ctc	ctc	tac	agg	1632
Ile	Gly	Thr	Leu	Val	Ala	Val	Leu	Ala	Ala	Ser	Ala	Leu	Leu	Tyr	Arg	
		370				375						380				
cac	tgg	att	gaa	ata	gtg	ctg	ctg	tac	cgg	acc	tac	cag	agc	aag	gat	1680
His	Trp	Ile	Glu	Ile	Val	Leu	Leu	Tyr	Arg	Thr	Tyr	Gln	Ser	Lys	Asp	
	385					390					395					
cag	acg	ctt	ggg	gat	aaa	aag	gat	ttt	gat	gct	ttc	gta	tcc	tat	gca	1728
Gln	Thr	Leu	Gly	Asp	Lys	Lys	Asp	Phe	Asp	Ala	Phe	Val	Ser	Tyr	Ala	
400					405					410					415	
aaa	tgg	agc	tct	ttt	cca	agt	gag	gcc	act	tca	tct	ctg	agt	gaa	gaa	1776
Lys	Trp	Ser	Ser	Phe	Pro	Ser	Glu	Ala	Thr	Ser	Ser	Leu	Ser	Glu	Glu	
				420					425					430		
cac	ttg	gcc	ctg	agc	cta	ttt	cct	gat	gtt	tta	gaa	aac	aaa	tat	gga	1824
His	Leu	Ala	Leu	Ser	Leu	Phe	Pro	Asp	Val	Leu	Glu	Asn	Lys	Tyr	Gly	
			435					440					445			
tat	agc	ctg	tgt	ttg	ctt	gaa	aga	gat	gtg	gct	cca	gga	gga	gtg	tat	1872
Tyr	Ser	Leu	Cys	Leu	Leu	Glu	Arg	Asp	Val	Ala	Pro	Gly	Gly	Val	Tyr	
		450					455					460				
gca	gaa	gac	att	gtg	agc	att	att	aag	aga	agc	aga	aga	gga	ata	ttt	1920
Ala	Glu	Asp	Ile	Val	Ser	Ile	Ile	Lys	Arg	Ser	Arg	Arg	Gly	Ile	Phe	

465	470	475	
atc ttg agc ccc aac tat gtc aat gga ccc agt atc ttt gaa cta caa Ile Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln 480 485 490 495			1968
gca gca gtg aat ctt gcc ttg gat gat caa aca ctg aaa ctc att tta Ala Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu 500 505 510			2016
att aag ttc tgt tac ttc caa gag cca gag tct cta cct cat ctc gtg Ile Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val 515 520 525			2064
aaa aaa gct ctc agg gtt ttg ccc aca gtt act tgg aga ggc tta aaa Lys Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys 530 535 540			2112
tca gtt cct ccc aat tct agg ttc tgg gcc aaa atg cgc tac cac atg Ser Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met 545 550 555			2160
cct gtg aaa aac tct cag gga ttc acg tgg aac cag ctc aga att acc Pro Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr 560 565 570 575			2208
tct agg att ttt cag tgg aaa gga ctc agt aga aca gaa acc act ggg Ser Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly 580 585 590			2256
agg agc tcc cag cct aag gaa tgg tga aatgagccct ggagccccct Arg Ser Ser Gln Pro Lys Glu Trp 595			2303
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gttcaggctg ataggaaatt caaagagtct cctgccagca ccaagcaagc ttgatggaca			2423
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 <211> 599
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<400> 7

Met	Leu	Cys	Leu	Gly	Trp	Ile	Phe	Leu	Trp	Leu	Val	Ala	Gly	Glu	Arg
1				5					10					15	

Ile Lys Gly Phe Asn Ile Ser Gly Cys Ser Thr Lys Lys Leu Leu Trp

20	25	30
Thr Tyr Ser Thr Arg Ser Glu Glu Glu Phe Val Leu Phe Cys Asp Leu		
35	40	45
Pro Glu Pro Gln Lys Ser His Phe Cys His Arg Asn Arg Leu Ser Pro		
50	55	60
Lys Gln Val Pro Glu His Leu Pro Phe Met Gly Ser Asn Asp Leu Ser		
65	70	75
Asp Val Gln Trp Tyr Gln Gln Pro Ser Asn Gly Asp Pro Leu Glu Asp		
85	90	95
Ile Arg Lys Ser Tyr Pro His Ile Ile Gln Asp Lys Cys Thr Leu His		
100	105	110
Phe Leu Thr Pro Gly Val Asn Asn Ser Gly Ser Tyr Ile Cys Arg Pro		
115	120	125
Lys Met Ile Lys Ser Pro Tyr Asp Val Ala Cys Cys Val Lys Met Ile		
130	135	140
Leu Glu Val Lys Pro Gln Thr Asn Ala Ser Cys Glu Tyr Ser Ala Ser		
145	150	155
His Lys Gln Asp Leu Leu Leu Gly Ser Thr Gly Ser Ile Ser Cys Pro		
165	170	175
Ser Leu Ser Cys Gln Ser Asp Ala Gln Ser Pro Ala Val Thr Trp Tyr		
180	185	190
Lys Asn Gly Lys Leu Leu Ser Val Glu Arg Ser Asn Arg Ile Val Val		
195	200	205
Asp Glu Val Tyr Asp Tyr His Gln Gly Thr Tyr Val Cys Asp Tyr Thr		
210	215	220
Gln Ser Asp Thr Val Ser Ser Trp Thr Val Arg Ala Val Val Gln Val		
225	230	235
Arg Thr Ile Val Gly Asp Thr Lys Leu Lys Pro Asp Ile Leu Asp Pro		
245	250	255
Val Glu Asp Thr Leu Glu Val Glu Leu Gly Lys Pro Leu Thr Ile Ser		
260	265	270

Cys Lys Ala Arg Phe Gly Phe Glu Arg Val Phe Asn Pro Val Ile Lys
 275 280 285

Trp Tyr Ile Lys Asp Ser Asp Leu Glu Trp Glu Val Ser Val Pro Glu
 290 295 300

Ala Lys Ser Ile Lys Ser Thr Leu Lys Asp Glu Ile Ile Glu Arg Asn
 305 310 315 320

Ile Ile Leu Glu Lys Val Thr Gln Arg Asp Leu Arg Arg Lys Phe Val
 325 330 335

Cys Phe Val Gln Asn Ser Ile Gly Asn Thr Thr Gln Ser Val Gln Leu
 340 345 350

Lys Glu Lys Arg Gly Val Val Leu Leu Tyr Ile Leu Leu Gly Thr Ile
 355 360 365

Gly Thr Leu Val Ala Val Leu Ala Ala Ser Ala Leu Leu Tyr Arg His
 370 375 380

Trp Ile Glu Ile Val Leu Leu Tyr Arg Thr Tyr Gln Ser Lys Asp Gln
 385 390 395 400

Thr Leu Gly Asp Lys Lys Asp Phe Asp Ala Phe Val Ser Tyr Ala Lys
 405 410 415

Trp Ser Ser Phe Pro Ser Glu Ala Thr Ser Ser Leu Ser Glu Glu His
 420 425 430

Leu Ala Leu Ser Leu Phe Pro Asp Val Leu Glu Asn Lys Tyr Gly Tyr
 435 440 445

Ser Leu Cys Leu Leu Glu Arg Asp Val Ala Pro Gly Gly Val Tyr Ala
 450 455 460

Glu Asp Ile Val Ser Ile Ile Lys Arg Ser Arg Arg Gly Ile Phe Ile
 465 470 475 480

Leu Ser Pro Asn Tyr Val Asn Gly Pro Ser Ile Phe Glu Leu Gln Ala
 485 490 495

Ala Val Asn Leu Ala Leu Asp Asp Gln Thr Leu Lys Leu Ile Leu Ile
 500 505 510

Lys Phe Cys Tyr Phe Gln Glu Pro Glu Ser Leu Pro His Leu Val Lys
 515 520 525

Lys Ala Leu Arg Val Leu Pro Thr Val Thr Trp Arg Gly Leu Lys Ser
 530 535 540

Val Pro Pro Asn Ser Arg Phe Trp Ala Lys Met Arg Tyr His Met Pro
 545 550 555 560

Val Lys Asn Ser Gln Gly Phe Thr Trp Asn Gln Leu Arg Ile Thr Ser
 565 570 575

Arg Ile Phe Gln Trp Lys Gly Leu Ser Arg Thr Glu Thr Thr Gly Arg
 580 585 590

Ser Ser Gln Pro Lys Glu Trp
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<212> PRT

<213> Artificial Sequence

<220>

<223> Flag peptide

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Asp Tyr Lys Asp Asp Asp Asp Lys
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